

## IN THE CLAIMS:

1. (currently amended) A method for identifying a molecule that modulates the biological activity of a native quadruplex DNA, which comprises  
contacting a test quadruplex DNA with a candidate molecule, wherein the test quadruplex DNA comprises the nucleotide sequence (GGA)<sub>4</sub> (SEQ ID NO:1) or the nucleotide sequence (GGA)<sub>3</sub>GG (SEQ ID NO:2), and wherein G is guanine and A is adenine; and  
determining the presence or absence of an interaction between the candidate molecule and the test quadruplex DNA, whereby the candidate molecule that interacts with the test quadruplex DNA is identified as the molecule that modulates the biological activity of the native quadruplex DNA.

2. (currently amended) The method of claim 1, wherein the test quadruplex DNA comprises a nucleotide sequence selected from the group consisting of

(GGA)<sub>4</sub>AGA(GGA)<sub>3</sub>GGC (SEQ ID NO:15);  
(GGA)<sub>4</sub> (SEQ ID NO:1);  
AGAGAAGAGG(GGA)<sub>3</sub>GAGGAGGAGGCGC (SEQ ID NO:16);  
GGAGGGGGAGGGG (SEQ ID NO:17);  
AGGAGAA(GGA)<sub>2</sub>GGT(GGA)<sub>3</sub>G<sub>3</sub> (SEQ ID NO:18);  
(GGA)<sub>3</sub>AGAATGCGA(GGA)<sub>2</sub>G<sub>3</sub>AGGAG (SEQ ID NO:19);  
CCGAA(GGA)<sub>2</sub>A(GGA)<sub>3</sub>G<sub>4</sub> (SEQ ID NO:20);  
(GGA)<sub>2</sub>CCGA(GGA)<sub>2</sub> (SEQ ID NO:25);  
GGAA(GGA)<sub>3</sub> (SEQ ID NO:23);  
AGAAGAG(GGA)<sub>3</sub>G (SEQ ID NO:22); and  
AGCGA(GGA)<sub>8</sub>GAGGAA (SEQ ID NO:21)

3. (previously presented) The method of claim 1, wherein the test quadruplex DNA comprises a nucleotide sequence that is identical to a nucleotide sequence in native quadruplex DNA.

4. (previously presented) The method of claim 1, wherein the test quadruplex DNA comprises a nucleotide sequence that is identical to a gene transcription regulatory nucleotide sequence in native quadruplex DNA.
5. (previously presented) The method of claim 1, wherein the test quadruplex DNA is in a heptad/tetrad conformation.
6. (previously presented) The method of claim 5, wherein the heptad/tetrad conformation of the test quadruplex DNA is formed by incubating the DNA in a solution comprising potassium ions for a time period less than the time period required to form another quadruplex conformation.
7. (previously presented) The method of claim 5, wherein the test quadruplex DNA comprises a mutation that hinders formation of another quadruplex conformation.
8. (previously presented) The method of claim 1, wherein the test quadruplex DNA is coupled to a reporter expression system.
9. (previously presented) The method of claim 8, wherein the reporter expression system comprises a luciferase reporter.
10. (previously presented) The method of claim 1, wherein the interaction is assayed by a Taq polymerase arrest assay.
11. (previously presented) The method of claim 1, wherein the interaction is a binding interaction.
12. (currently amended) A method for modulating the biological activity of a biologically significant native quadruplex DNA, which comprises contacting a system comprising the native quadruplex DNA with a molecule that interacts with quadruplex DNA comprising the nucleotide sequence (GGA)<sub>4</sub> (SEQ ID NO:1) or the nucleotide sequence

(GGA)<sub>3</sub>GG (SEQ ID NO:2), wherein G is guanine and A is adenine; whereby the molecule modulates the biological activity of the native quadruplex DNA.

13. (currently amended) The method of claim 12, wherein the native quadruplex DNA comprises a nucleotide sequence selected from the group consisting of

(GGA)<sub>4</sub>AGA(GGA)<sub>3</sub>GGC (SEQ ID NO:15);  
(GGA)<sub>4</sub> (SEQ ID NO:1);  
AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16);  
GGAGGGGGAGGGG (SEQ ID NO:17);  
AGGAGAA(GGA)<sub>2</sub>GGT(GGA)<sub>3</sub>G<sub>3</sub> (SEQ ID NO:18);  
(GGA)<sub>3</sub>AGAATGCGA(GGA)<sub>2</sub>G<sub>3</sub>AGGAG (SEQ ID NO:19);  
CCGAA(GGA)<sub>2</sub>A(GGA)<sub>3</sub>G<sub>4</sub> (SEQ ID NO:20);  
(GGA)<sub>2</sub>CCGA(GGA)<sub>2</sub> (SEQ ID NO:25);  
GGAA(GGA)<sub>3</sub> (SEQ ID NO:23);  
AGAAGAG(GGA)<sub>3</sub>G (SEQ ID NO:22); and  
AGCGA(GGA)<sub>8</sub>GAGGAA (SEQ ID NO:21).

14. (previously presented) The method of claim 12, wherein the test quadruplex DNA is in a heptad/tetrad conformation.

15. (previously presented) The method of claim 14, wherein the heptad/tetrad conformation of the test quadruplex DNA is formed by incubating the DNA in a solution comprising potassium ions for a time period less than the time period required to form another quadruplex conformation.

16. (previously presented) The method of claim 14, wherein the test quadruplex DNA comprises a mutation that hinders formation of another quadruplex conformation.

17. (previously presented) The method of claim 12, wherein the system is a cell.

18. (previously presented) The method of claim 12, wherein the system is an organism.

19. (previously presented) A method for identifying a quadruplex structure in a nucleic acid of a sample, which comprises contacting the sample with a quadruplex-interacting agent and detecting the presence or absence of an interaction between the nucleic acid and the quadruplex-interacting agent, whereby the presence of an interaction is indicative of the quadruplex structure in the nucleic acid.

20. (previously presented) The method of claim 19, wherein the quadruplex-interacting agent is TMPyP4 or telomestatin.

21. (previously presented) The method of claim 19, wherein the quadruplex structure is in a heptad/tetrad conformation.

22. (currently amended) A method for identifying a nucleotide sequence capable of forming a quadruplex structure, which comprises identifying in a database a subset of nucleotide sequences comprising (GGA)<sub>4</sub> (SEQ ID NO:1), (GGA)<sub>3</sub>GG (SEQ ID NO:2) or (GGA)<sub>3</sub>GGX<sub>n</sub>(GGA)<sub>3</sub>GG, wherein n is an integer between 0 and 3 (SEQ ID NOS:3-6).

23. (previously presented) The method of claim 22, which further comprises identifying nucleotide sequences from the subset of nucleotide sequences adjacent to a gene coding region.

24. (previously presented) The method of claim 22, which further comprises identifying nucleotide sequences from the subset of nucleotide sequences identical to or substantially identical to an oncogene nucleotide sequence.

25. (currently amended) A method for identifying a nucleotide sequence capable of forming a quadruplex structure, which comprises contacting a cell with a quadruplex interacting agent, identifying a subset of RNA nucleotide sequences increased or decreased 2-fold or more in the cell as compared to a cell not contacted with the quadruplex interacting agent, and identifying a nucleotide sequence from the subset comprising (GGA)<sub>4</sub> (SEQ ID NO:1),

(GGA)<sub>3</sub>GG (SEQ ID NO:2) or (GGA)<sub>3</sub>GGX<sub>n</sub>(GGA)<sub>3</sub>GG (SEQ ID NO:4) as the nucleotide sequence capable of forming a quadruplex structure.

26. (previously presented)The method of claim 25, wherein the quadruplex interacting agent is TMPyP4 or telomestatin.